

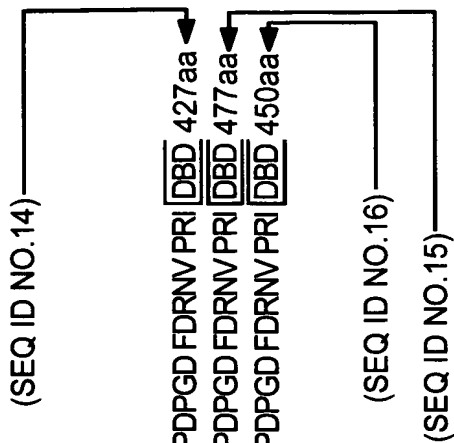
A

Exons: 1f 1e 1a 1d 1b 1c 2 3 4 5 6 7 8 9

Cosmids: J5 AE D2 WE



FIG. 1C



Transcript 1:

Transcript 6:

Transcript 9:



FIG. 4

- A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC
CGTGACATTGCTTTGCTTGCCCTCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtaag...3' (SEQ ID NO: 13)
- B. 5'...TGCGACCTTGCGGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGAAGCAGGGGCGCCCAAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCTCCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)
- C. 5'...tgtttttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3' (SEQ ID NO: 6)
- D. 5'...GTTTCCTTCTTCTGTGCGGGGCGCCTTGGCAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTGATGGTGCTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3' (SEQ ID NO: 1)



FIG. 5A

Transcript 6

(Sequence Range: 1 to 1463)

```

      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                               MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

     110     120     130     140     150
      *      *      *      *      *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

     160     170     180     190     200
      *      *      *      *      *
CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

     210     220     230     240     250
      *      *      *      *      *
ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAACTG GCCTTGACAG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

     260     270     280     290     300
      *      *      *      *      *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
ACCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

     310     320     330     340     350
      *      *      *      *      *
GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
CACTTCCGAC GTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

     360     370     380     390     400
      *      *      *      *      *
TTCACCTGCC CCTTCAACGG GGAAGTCCGC ATCACCAAGG ACAACCGACG
AAGTGGACCG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>

```



FIG. 5B

```

      410      420      430      440      450
      *      *      *      *      *
CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
GGTGACGGTC CGGACGGCCG AGTTTGCAGC ACACCTGTAG CCGTACTACT
HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

      460      470      480      490      500
      *      *      *      *      *
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

      510      520      530      540      550
      *      *      *      *      *
CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
GACTTCGCCT TCCTCCTCCT CCGGAACCTC CTGTCAGACG CCGGGTTCGA
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

      560      570      580      590      600
      *      *      *      *      *
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

      610      620      630      640      650
      *      *      *      *      *
AGACCTACGA CCCACCTAC TCCGACTTCT GCCAGTTCCT GCCTCCAGTT
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CCGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

      660      670      680      690      700
      *      *      *      *      *
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

      710      720      730      740      750
      *      *      *      *      *
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
GTGAGGGTCTG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

      760      770      780      790      800
      *      *      *      *      *
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

      810      820      830      840      850
      *      *      *      *      *
AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
TCACCTCTTC TAAGTCTACT GGGGAAGACAC TGGGATCTCG ACAGGGTCTGA
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>

```



FIG. 5C

```
      860      870      880      890      900
      *      *      *      *      *
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTC
SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>

      910      920      930      940      950
      *      *      *      *      *
TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>

      960      970      980      990     1000
      *      *      *      *      *
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>

     1010     1020     1030     1040     1050
      *      *      *      *      *
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>

     1060     1070     1080     1090     1100
      *      *      *      *      *
AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

     1110     1120     1130     1140     1150
      *      *      *      *      *
GAGCTGATTG AGCCCCTCAT CAAGTTCAG GTGGGACTGA AGAAGCTGAA
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

     1160     1170     1180     1190     1200
      *      *      *      *      *
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

     1210     1220     1230     1240     1250
      *      *      *      *      *
CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCTTG
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

     1260     1270     1280     1290     1300
      *      *      *      *      *
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>
```



FIG. 5D

```
      1310      1320      1330      1340      1350
      *      *      *      *      *      *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTCTACTA GGTCTTCGAT CGGCTGGACG
GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

      1360      1370      1380      1390      1400
      *      *      *      *      *      *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

      1410      1420      1430      1440      1450
      *      *      *      *      *      *
CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA
GGA CTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

      1460
      *      *
TGAGATCTCC TGA (SEQ ID NO:2)
ACTCTAGAGG ACT (SEQ ID NO:17)
GluIleSer ***>(SEQ ID NO:9)
```



FIG. 6A

Transcript 9

(Sequence range: 1 to 1382)

```

      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCTGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                               MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTCTGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

     110     120     130     140     150
      *      *      *      *      *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
    GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

     160     170     180     190     200
      *      *      *      *      *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

     210     220     230     240     250
      *      *      *      *      *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

     260     270     280     290     300
      *      *      *      *      *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
    MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

     310     320     330     340     350
      *      *      *      *      *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTTCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

     360     370     380     390     400
      *      *      *      *      *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>

```




FIG. 6B

```

      410      420      430      440      450
      *      *      *      *      *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACCTCC
ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

      460      470      480      490      500
      *      *      *      *      *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

      510      520      530      540      550
      *      *      *      *      *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

      560      570      580      590      600
      *      *      *      *      *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

      610      620      630      640      650
      *      *      *      *      *
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

      660      670      680      690      700
      *      *      *      *      *
TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

      710      720      730      740      750
      *      *      *      *      *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

      760      770      780      790      800
      *      *      *      *      *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

      810      820      830      840      850
      *      *      *      *      *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
TCAATGTCGT AGGTTTTCCTA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>

```



FIG. 6C

```
      860      870      880      890      900
      *      *      *      *      *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
  ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>

      910      920      930      940      950
      *      *      *      *      *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>

      960      970      980      990     1000
      *      *      *      *      *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>

     1010     1020     1030     1040     1050
      *      *      *      *      *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
  LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>

     1060     1070     1080     1090     1100
      *      *      *      *      *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>

     1110     1120     1130     1140     1150
      *      *      *      *      *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>

     1160     1170     1180     1190     1200
      *      *      *      *      *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
  IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>

     1210     1220     1230     1240     1250
      *      *      *      *      *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>

     1260     1270     1280     1290     1300
      *      *      *      *      *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>
```



Title: Isoforms of the Human Vitamin D Receptor
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Docket No.: RICE-014

FIG. 6D

1310	1320	1330	1340	1350
* *	* *	* *	* *	* *
CCGCTGCCTC	TCCTTCCAGC	CTGAGTGCAG	CATGAAGCTA	ACGCCCCCTTG
GGCGACGGAG	AGGAAGGTCG	GACTCACGTC	GTACTTCGAT	TGCGGGGAAC
ArgCysLeu	SerPheGln	ProGluCysSer	MetLysLeu	ThrProLeu>
1360	1370	1380		
* *	* *	* *		
TGCTCGAAGT	GTTTGGCAAT	GAGATCTCCT	GA	(SEQ ID NO:3)
ACGAGCTTCA	CAAACCGTTA	CTCTAGAGGA	CT	(SEQ ID NO:18)
ValLeuGluVal	PheGlyAsn	GluIleSer	***>	(SEQ ID NO:10)



FIG. 7A

Transcript 10

(Sequence Range: 1 to 1534)

```

      10      20      30      40      50
      *      *      *      *      *      *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                               MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *      *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

     110     120     130     140     150
      *      *      *      *      *      *
GGAGGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

     160     170     180     190     200
      *      *      *      *      *      *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

     210     220     230     240     250
      *      *      *      *      *      *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg*** (SEQ ID NO:11)

     260     270     280     290     300
      *      *      *      *      *      *
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC

     310     320     330     340     350
      *      *      *      *      *      *
TTTCCATGAA GGGAGCCCTT GCATTTTTCa CATCTCCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

     360     370     380     390     400
      *      *      *      *      *      *
CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA
GGTACCTTGT ACGCCGCGAG TGTCGGTGTC CTCGTCCTCC CAGAACCGCT
```



FIG. 7B

410	420	430	440	450
* *	* *	* *	* *	* *
AGCATGAAGC	GGAAGGCACT	ATTCACCTGC	CCCTTCAACG	GGGACTGCCG
TCGTACTTCG	CCTTCCGTGA	TAAGTGGACG	GGGAAGTTGC	CCCTGACGGC
460	470	480	490	500
* *	* *	* *	* *	* *
CATCACCAAG	GACAACCGAC	GCCACTGCCA	GGCCTGCCGG	CTCAAACGCT
GTAGTGGTTC	CTGTTGGCTG	CGGTGACGGT	CCGGACGGCC	GAGTTTGCGA
510	520	530	540	550
* *	* *	* *	* *	* *
GTGTGGACAT	CGGCATGATG	AAGGAGTTCA	TTCTGACAGA	TGAGGAAGTG
CACACCTGTA	GCCGTACTAC	TTCCTCAAGT	AAGACTGTCT	ACTCCTTCAC
560	570	580	590	600
* *	* *	* *	* *	* *
CAGAGGAAGC	GGGAGATGAT	CCTGAAGCGG	AAGGAGGAGG	AGGCCTTGAA
GTCTCCTTCG	CCCTCTACTA	GGACTTCGCC	TTCCTCCTCC	TCCGGAACCTT
610	620	630	640	650
* *	* *	* *	* *	* *
GGACAGTCTG	CGGCCCAAGC	TGTCTGAGGA	GCAGCAGCGC	ATCATTGCCA
CCTGTCAGAC	GCCGGGTTCG	ACAGACTCCT	CGTCGTCGCG	TAGTAACGGT
660	670	680	690	700
* *	* *	* *	* *	* *
TACTGCTGGA	CGCCCACCAT	AAGACCTACG	ACCCACCTA	CTCCGACTTC
ATGACGACCT	GCGGGTGGTA	TTCTGGATGC	TGGGGTGGAT	GAGGCTGAAG
710	720	730	740	750
* *	* *	* *	* *	* *
TGCCAGTTCC	GGCCTCCAGT	TCGTGTGAAT	GATGGTGGAG	GGAGCCATCC
ACGGTCAAGG	CCGGAGGTCA	AGCACACTTA	CTACCACCTC	CCTCGGTAGG
760	770	780	790	800
* *	* *	* *	* *	* *
TTCCAGGCCC	AACTCCAGAC	ACACTCCCAG	CTTCTCTGGG	GACTCCTCCT
AAGGTCCGGG	TTGAGGTCTG	TGTGAGGGTC	GAAGAGACCC	CTGAGGAGGA
810	820	830	840	850
* *	* *	* *	* *	* *
CCTCCTGCTC	AGATCACTGT	ATCACCTCTT	CAGACATGAT	GGACTCGTCC
GGAGGACGAG	TCTAGTGACA	TAGTGGAGAA	GTCTGTACTA	CCTGAGCAGG
860	870	880	890	900
* *	* *	* *	* *	* *
AGCTTCTCCA	ATCTGGATCT	GAGTGAAGAA	GATTCAGATG	ACCCTTCTGT
TCGAAGAGGT	TAGACCTAGA	CTCACTTCTT	CTAAGTCTAC	TGGGAAGACA
910	920	930	940	950
* *	* *	* *	* *	* *
GACCCTAGAG	CTGTCCCAGC	TCTCCATGCT	GCCCCACCTG	GCTGACCTGG
CTGGGATCTC	GACAGGGTCG	AGAGGTACGA	CGGGGTGGAC	CGACTGGACC



FIG. 7C

960	970	980	990	1000
* *	* *	* *	* *	* *
TCAGTTACAG	CATCCAAAAG	GTCATTGGCT	TTGCTAAGAT	GATACCAGGA
AGTCAATGTC	GTAGGTTTTTC	CAGTAACCGA	AACGATTCTA	CTATGGTCCCT
1010	1020	1030	1040	1050
* *	* *	* *	* *	* *
TTCAGAGACC	TCACCTCTGA	GGACCAGATC	GTACTGCTGA	AGTCAAGTGC
AAGTCTCTGG	AGTGGAGACT	CCTGGTCTAG	CATGACGACT	TCAGTTCACG
1060	1070	1080	1090	1100
* *	* *	* *	* *	* *
CATTGAGGTC	ATCATGTTGC	GCTCCAATGA	GTCCTTCACC	ATGGACGACA
GTAACCTCCAG	TAGTACAACG	CGAGGTTACT	CAGGAAGTGG	TACCTGCTGT
1110	1120	1130	1140	1150
* *	* *	* *	* *	* *
TGTCCCTGGAC	CTGTGGCAAC	CAAGACTACA	AGTACCGCGT	CAGTGACGTG
ACAGGACCTG	GACACCGTTG	GTTCTGATGT	TCATGGCGCA	GTCACTGCAC
1160	1170	1180	1190	1200
* *	* *	* *	* *	* *
ACCAAAGCCG	GACACAGCCT	GGAGCTGATT	GAGCCCCTCA	TCAAGTTCCA
TGGTTTCGGC	CTGTGTCGGA	CCTCGACTAA	CTCGGGGAGT	AGTTCAAGGT
1210	1220	1230	1240	1250
* *	* *	* *	* *	* *
GGTGGGACTG	AAGAAGCTGA	ACTTGCAATGA	GGAGGAGCAT	GTCCTGCTCA
CCACCCTGAC	TTCTTCGACT	TGAACGTACT	CCTCCTCGTA	CAGGACGAGT
1260	1270	1280	1290	1300
* *	* *	* *	* *	* *
TGGCCATCTG	CATCGTCTCC	CCAGATCGTC	CTGGGGTGCA	GGACGCCGCG
ACCGGTAGAC	GTAGCAGAGG	GGTCTAGCAG	GACCCACGCT	CCTGCGGCGC
1310	1320	1330	1340	1350
* *	* *	* *	* *	* *
CTGATTGAGG	CCATCCAGGA	CCGCCTGTCC	AACACACTGC	AGACGTACAT
GACTAACTCC	GGTAGGTCCT	GGCGGACAGG	TTGTGTGACG	TCTGCATGTA
1360	1370	1380	1390	1400
* *	* *	* *	* *	* *
CCGCTGCCGC	CACCCGCCCC	CGGGCAGCCA	CCTGCTCTAT	GCCAAGATGA
GGCGACGGCG	GTGGGCGGGG	GCCCGTCGGT	GGACGAGATA	CGGTTCTACT
1410	1420	1430	1440	1450
* *	* *	* *	* *	* *
TCCAGAAGCT	AGCCGACCTG	CGCAGCCTCA	ATGAGGAGCA	CTCCAAGCAG
AGGTCTTCGA	TCGGCTGGAC	GCGTCGGAGT	TACTCCTCGT	GAGGTTTCGT
1460	1470	1480	1490	1500
* *	* *	* *	* *	* *
TACCGCTGCC	TCTCCTTCCA	GCCTGAGTGC	AGCATGAAGC	TAACGCCCCCT
ATGGCGACGG	AGAGGAAGGT	CGGACTCACG	TCGTACTTCG	ATTGCGGGGA



Title: Isoforms of the Human Vitamin D Receptor
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Docket No.: RICE-014

FIG. 7D

1510	1520	1530
* *	* *	* *
TGTGCTCGAA	GTGTTTGGCA	ATGAGATCTC
CTGA (SEQ ID NO: 4)		
ACACGAGCTT	CACAAACCGT	TACTCTAGAG
GACT (SEQ ID NO: 19)		



FIG. 8A

10 *	20 *	30 *	40 *	50 *
TGCGACCTTG	GCGGTGAGCC	TGGGGACAGG	GGTGAGGCCA	GAGACGGACG
ACGCTGGAAC	CGCCACTCGG	ACCCCTGTCC	CCACTCCGGT	CTCTGCCTGC
60 *	70 *	80 *	90 *	100 *
GACGCAGGGG	CCCGGCCCAA	GGCGAGGGAG	AACAGCGGCA	CTAAGGCAGA
CTGCGTCCCC	GGGCCGGGTT	CCGCTCCCTC	TTGTCGCCGT	GATTCCGTCT
110 *	120 *	130 *	140 *	150 *
AAGGAAGAGG	GCGGTGTGTT	CACCCGCAGC	CCAATCCATC	ACTCAGCAAC
TTCTTCTCC	CGCCACACAA	GTGGGCGTCG	GGTTAGGTAG	TGAGTCGTTG
160 *	170 *	180 *	190 *	200 *
TCCTAGACGC	TGGTAGAAAG	TTCCTCCGAG	GAGCCTGCCA	TCCAGTCGTG
AGGATCTGCG	ACCATCTTTC	AAGGAGGCTC	CTCGGACGGT	AGGTCAGCAC
210 *	220 *	230 *	240 *	250 *
CGTGCAAGAAG	CCTTTGGGTC	TGAAGTGTCT	GTGAGACCTC	ACAGAAGAGC
GCACGTCTTC	GGAAACCCAG	ACTTCACAGA	CACTCTGGAG	TGTCTTCTCG
260 *	270 *	280 *	290 *	300 *
ACCCCTGGGC	TCCACTTACC	TGCCCCCTGC	TCCTTCAGGG	ATGGAGGCAA
TGGGGACCCG	AGGTGAATGG	ACGGGGGACG	AGGAAGTCCC	TACCTCCGTT
				MetGluAla>
310 *	320 *	330 *	340 *	350 *
TGGCGGCCAG	CACTTCCCTG	CCTGACCCTG	GAGACTTTGA	CCGGAACGTG
ACCGCCGGTC	GTGAAGGGAC	GGACTGGGAC	CTCTGAAACT	GGCCTTGCAC
MetAlaAlaSer	ThrSerLeu	ProAspPro	GlyAspPheAsp	ArgAsnVal>
360 *	370 *	380 *	390 *	400 *
CCCCGGATCT	GTGGGGTGTG	TGGAGACCGA	GCCACTGGCT	TTCACTTCAA
GGGGCCTAGA	CACCCACAC	ACCTCTGGCT	CGGTGACCGA	AAGTGAAGTT
ProArgIle	CysGlyValCys	GlyAspArg	AlaThrGly	PheHisPheAsn>
410 *	420 *	430 *	440 *	450 *
TGCTATGACC	TGTGAAGGCT	GCAAAGGCTT	CTTCAGGCCA	AGCATGAAGC
ACGATACTGG	ACACTTCCGA	CGTTTCCGAA	GAAGTCCGCT	TCGTACTTCG
AlaMetThr	CysGluGly	CysLysGlyPhe	PheArgArg	SerMetLys>
460 *	470 *	480 *	490 *	500 *
GGAAGGCACT	ATTCACCTGC	CCCTTCAACG	GGGACTGCCG	CATCACCAAG
CCTTCCGTGA	TAAGTGGACG	GGGAAGTTGC	CCCTGACGGC	GTAAGTGGTTC
ArgLysAlaLeu	PheThrCys	ProPheAsn	GlyAspCysArg	IleThrLys>



FIG. 8B

```
510      520      530      540      550
*        *        *        *        *
GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
CTGTTGGCTG CCGTGACGGT CCGGACGGCC GAGTTTGC GA CACACCTGTA
AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

560      570      580      590      600
*        *        *        *        *
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

610      620      630      640      650
*        *        *        *        *
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACCTT CCTGTCTAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

660      670      680      690      700
*        *        *        *        *
CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

710      720      730      740      750
*        *        *        *        *
CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

760      770      780      790      800
*        *        *        *        *
GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

810      820      830      840      850
*        *        *        *        *
AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

860      870      880      890      900
*        *        *        *        *
AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

910      920      930      940      950
*        *        *        *        *
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
TAGACCTAGA CTCATTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

960      970      980      990      1000
*        *        *        *        *
CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>
```



FIG. 8C

```

1010      1020      1030      1040      1050
  *          *          *          *          *
CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
GTAGGTTTTT CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
  IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

1060      1070      1080      1090      1100
  *          *          *          *          *
TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

1110      1120      1130      1140      1150
  *          *          *          *          *
ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCTGGAC
TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
  IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

1160      1170      1180      1190      1200
  *          *          *          *          *
CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
  CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

1210      1220      1230      1240      1250
  *          *          *          *          *
GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

1260      1270      1280      1290      1300
  *          *          *          *          *
AAGAAGCTGA ACTTGCA TGA GAGGAGCAT GTCCTGCTCA TGGCCATCTG
TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

1310      1320      1330      1340      1350
  *          *          *          *          *
CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
GTAGCAGAGG GTCTAGCAG GACCCACGCT CCTGCGGCGC GACTAACTCC
  IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

1360      1370      1380      1390      1400
  *          *          *          *          *
CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
GGTAGGTCTT GCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

1410      1420      1430      1440      1450
  *          *          *          *          *
CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
GTGGGCGGGG GCGGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

1460      1470      1480      1490      1500
  *          *          *          *          *
AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>

```



Title: Isoforms of the Human Vitamin D Receptor
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Docket No.: RICE-014

FIG. 8D

```
      1510      1520      1530      1540      1550
      *          *          *          *          *
TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCCT TGTGCTCGAA
AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

      1560      1570
      *          *
GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:7)
CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:20)
ValPheGly AsnGluIleSer ***> (SEQ ID NO:12)
```



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FIG 1 A.

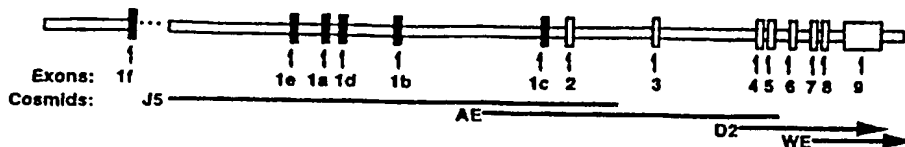


FIG 1 B.

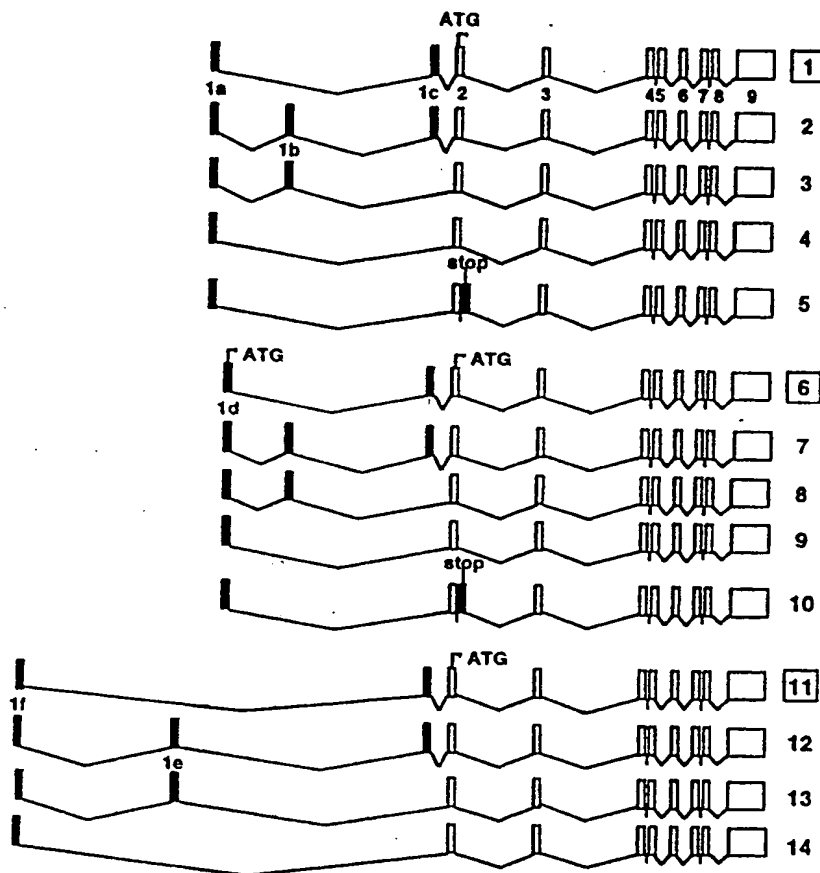


FIG 1c.

Transcript 1:

Transcript 6:

Transcript 9:

MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPIR RAPLG STYLP PAPSG
 MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPIR RAPLG STYLP PAPSG
 MEW RNNKR SDWLS MVLRT AGVEG

MEAMA ASTSL PDPGD FDRNV PRI DBD 427aa
 MEAMA ASTSL PDPGD FDRNV PRI DBD 477aa
 MEAMA ASTSL PDPGD FDRNV PRI DBD 450aa

427aa

477aa

450aa

(SEQ ID NO:14)

(SEQ ID NO:15)

FIGURE 1

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- A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCC
CGTGACATTGCTTTGCTTGCCTCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtacag...3' (SEQ ID NO: 13)
- B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGAACGAGGGGCCCGGCCCAAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCGACCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCTCTCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)
- C. 5'...tgtttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3' (SEQ ID NO: 6)
- D. 5'...GTTTCCTTCTTCTGTCTGGGGCGCCTTGGC ATG GAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTCTG ATG GTGCTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3' (SEQ ID NO: 11)

FIG. 4
~~FIGURE 4~~

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FIG. 5A
FIGURE 5

TRANSCRIPT 6

(Sequence Range: 1 to 1463)

```

      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCTGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                   MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTCTGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

     110     120     130     140     150
      *      *      *      *      *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

     160     170     180     190     200
      *      *      *      *      *
CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

     210     220     230     240     250
      *      *      *      *      *
ACTTCCCTGC CTGACCTTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAACTG GCCTTGACAG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

     260     270     280     290     300
      *      *      *      *      *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
ACCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

     310     320     330     340     350
      *      *      *      *      *
GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
CACTTCCGAC GTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

     360     370     380     390     400
      *      *      *      *      *
TTCACCTGCC CCTTCAACGG GGAAGTGGCC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>

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FIG 5B

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```

      410      420      430      440      450
      *      *      *      *      *
CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
GGTGACGGTC CGGACGGCCG AGTTTGCGAC ACACCTGTAG CCGTACTACT
HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

      460      470      480      490      500
      *      *      *      *      *
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

      510      520      530      540      550
      *      *      *      *      *
CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
GACTTCGCCT TCCTCCTCCT CCGGAAC TTCGTGACAGC CCGGGTTCGA
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

      560      570      580      590      600
      *      *      *      *      *
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

      610      620      630      640      650
      *      *      *      *      *
AGACCTACGA CCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

      660      670      680      690      700
      *      *      *      *      *
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

      710      720      730      740      750
      *      *      *      *      *
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

      760      770      780      790      800
      *      *      *      *      *
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
AGTGGAAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

      810      820      830      840      850
      *      *      *      *      *
AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
TCACTTCTTC TAAGTCTACT GGAAGACAC TGGGATCTCG ACAGGGTCGA
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>

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FIG 5C



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860	870	880	890	900
* *	* *	* *	* *	* *
CTCCATGCTG	CCCCACCTGG	CTGACCTGGT	CAGTTACAGC	ATCCAAAAGG
GAGGTACGAC	GGGGTGGACC	GA CTGGACCA	GTCAATGTCG	TAGGTTTTCC
SerMetLeu	ProHisLeu	AlaAspLeuVal	SerTyrSer	IleGlnLys>
910	920	930	940	950
* *	* *	* *	* *	* *
TCATTGGCTT	TGCTAAGATG	ATACCAGGAT	TCAGAGACCT	CACCTCTGAG
AGTAACCGAA	ACGATTCTAC	TATGGTCCTA	AGTCTCTGGA	GTGGAGACTC
ValIleGlyPhe	AlaLysMet	IleProGly	PheArgAspLeu	ThrSerGlu>
960	970	980	990	1000
* *	* *	* *	* *	* *
GACCAGATCG	TACTGCTGAA	GTCAAGTGCC	ATTGAGGTCA	TCATGTTGCG
CTGGTCTAGC	ATGACGACTT	CAGTTCACGG	TA ACTCCAGT	AGTACAACGC
AspGlnIle	ValLeuLeuLys	SerSerAla	IleGluVal	IleMetLeuArg>
1010	1020	1030	1040	1050
* *	* *	* *	* *	* *
CTCCAATGAG	TCCTTCACCA	TGGACGACAT	GTCCTGGACC	TGTGGCAACC
GAGGTTACTC	AGGAAGTGGT	ACCTGCTGTA	CAGGACCTGG	ACACCGTTGG
SerAsnGlu	SerPheThr	MetAspAspMet	SerTrpThr	CysGlyAsn>
1060	1070	1080	1090	1100
* *	* *	* *	* *	* *
AAGACTACAA	GTACCGCGTC	AGTGACGTGA	CCAAAGCCGG	ACACAGCCTG
TTCTGATGTT	CATGGCGCAG	TCACTGCACT	GGTTTCGGCC	TGTGTGCGAC
GlnAspTyrLys	TyrArgVal	SerAspVal	ThrLysAlaGly	HisSerLeu>
1110	1120	1130	1140	1150
* *	* *	* *	* *	* *
GAGCTGATTG	AGCCCCTCAT	CAAGTTCCAG	GTGGGACTGA	AGAAGCTGAA
CTCGACTAAC	TCGGGGAGTA	GTTCAAGGTC	CACCCTGACT	TCTTCGACTT
GluLeuIle	GluProLeuIle	LysPheGln	ValGlyLeu	LysLysLeuAsn>
1160	1170	1180	1190	1200
* *	* *	* *	* *	* *
CTTGCATGAG	GAGGAGCATG	TCCTGCTCAT	GGCCATCTGC	ATCGTCTCCC
GAACGTACTC	CTCCTCGTAC	AGGACGAGTA	CCGGTAGACG	TAGCAGAGGG
LeuHisGlu	GluGluHis	ValLeuLeuMet	AlaIleCys	IleValSer>
1210	1220	1230	1240	1250
* *	* *	* *	* *	* *
CAGATCGTCC	TGGGGTGCAG	GACGCCGCGC	TGATTGAGGC	CATCCAGGAC
GTCTAGCAGG	ACCCACGTC	CTGCGGCGCG	ACTAACTCCG	GTAGGTCCTG
ProAspArgPro	GlyValGln	AspAlaAla	LeuIleGluAla	IleGlnAsp>
1260	1270	1280	1290	1300
* *	* *	* *	* *	* *
CGCCTGTCCA	ACACACTGCA	GACGTACATC	CGCTGCCCGC	ACCCGCCCCC
GCGGACAGGT	TGTGTGACGT	CTGCATGTAG	GCGACGGCGG	TGGGCGGGGG
ArgLeuSer	AsnThrLeuGln	ThrTyrIle	ArgCysArg	HisProProPro>

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FIG 5D

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```

      1310      1320      1330      1340      1350
      *      *      *      *      *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTCTACTA GGTCTTCGAT CGGCTGGACG
GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

      1360      1370      1380      1390      1400
      *      *      *      *      *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

      1410      1420      1430      1440      1450
      *      *      *      *      *
CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

      1460
      *      *
TGAGATCTCC TGA (SEQ ID NO: 2)
ACTCTAGAGG ACT (SEQ ID NO: 17)
GluIleSer ***> (SEQ ID NO: 9)
```



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FIG. 6A

FIGURE 6

TRANSCRIPT 9

(Sequence Range: 1 to 1382)

```

      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

     110     120     130     140     150
      *      *      *      *      *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

     160     170     180     190     200
      *      *      *      *      *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGACGCG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

     210     220     230     240     250
      *      *      *      *      *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

     260     270     280     290     300
      *      *      *      *      *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

     310     320     330     340     350
      *      *      *      *      *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

     360     370     380     390     400
      *      *      *      *      *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>

```



FIG 6B

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```

      410      420      430      440      450
      *      *      *      *      *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACCTCC
ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

      460      470      480      490      500
      *      *      *      *      *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

      510      520      530      540      550
      *      *      *      *      *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

      560      570      580      590      600
      *      *      *      *      *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

      610      620      630      640      650
      *      *      *      *      *
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCTGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

      660      670      680      690      700
      *      *      *      *      *
TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

      710      720      730      740      750
      *      *      *      *      *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CTTTCTGTGA
GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

      760      770      780      790      800
      *      *      *      *      *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

      810      820      830      840      850
      *      *      *      *      *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
TCAATGTCGT AGGTTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>

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FIG 6C

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```
      860      870      880      890      900
      *      *      *      *      *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>

      910      920      930      940      950
      *      *      *      *      *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>

      960      970      980      990      1000
      *      *      *      *      *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>

      1010     1020     1030     1040     1050
      *      *      *      *      *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>

      1060     1070     1080     1090     1100
      *      *      *      *      *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCTGACTT CTTGACTTGG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>

      1110     1120     1130     1140     1150
      *      *      *      *      *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCACGTCC TGCGGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>

      1160     1170     1180     1190     1200
      *      *      *      *      *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>

      1210     1220     1230     1240     1250
      *      *      *      *      *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>

      1260     1270     1280     1290     1300
      *      *      *      *      *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>
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FIG 6D 12/20



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      1310      1320      1330      1340      1350
      *      *      *      *      *      *      *
CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG
GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TCGGGGAAC
ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

      1360      1370      1380
      *      *      *      *      *      *
TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO:3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO:18)
ValLeuGluVal PheGlyAsn GluIleSer ***> (SEQ ID NO:10)
```



FIG 7A

FIGURE 7

TRANSCRIPT 10

(Sequence Range: 1 to 1534)

```

      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCCTT
                               MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

     110     120     130     140     150
      *      *      *      *      *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCTG GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

     160     170     180     190     200
      *      *      *      *      *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGACACG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

     210     220     230     240     250
      *      *      *      *      *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg***

     260     270     280     290     300
      *      *      *      *      *
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCTCTTC TTCGTTCCAC

     310     320     330     340     350
      *      *      *      *      *
TTTCCATGAA GGGAGCCCTT GCATTTTTCa CATCTCCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

     360     370     380     390     400
      *      *      *      *      *
CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGCGGA
GGTACCTTGT ACGCCGCGAG TGTCGGTGTG CTCGTCCTCC CAGAACCGCT

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FIG 7B

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410	420	430	440	450
* *	* *	* *	* *	* *
AGCATGAAGC	GGAAGGCACT	ATTCACCTGC	CCCTTCAACG	GGGACTGCCG
TCGTACTTCG	CCTTCCGTGA	TAAGTGGACG	GGGAAGTTGC	CCCTGACGGC
460	470	480	490	500
* *	* *	* *	* *	* *
CATCACCAAG	GACAACCGAC	GCCACTGCCA	GGCCTGCCGG	CTCAAACGCT
GTAGTGGTTC	CTGTTGGCTG	CGGTGACGGT	CCGGACGGCC	GAGTTTGC GA
510	520	530	540	550
* *	* *	* *	* *	* *
GTGTGGACAT	CGGCATGATG	AAGGAGTTCA	TTCTGACAGA	TGAGGAAAGTG
CACACCTGTA	GCCGTACTAC	TTCTCAAGT	AAGACTGTCT	ACTCCTTCAC
560	570	580	590	600
* *	* *	* *	* *	* *
CAGAGGAAGC	GGGAGATGAT	CCTGAAGCGG	AAGGAGGAGG	AGGCCTTGAA
GTCTCCTTCG	CCCTCTACTA	GGACTTCGCC	TTCTCCTCCT	TCCGGAACCT
610	620	630	640	650
* *	* *	* *	* *	* *
GGACAGTCTG	CGGCCCAAGC	TGTCTGAGGA	GCAGCAGCGC	ATCATTTGCCA
CCTGTCAGAC	GCCGGGTTCG	ACAGACTCCT	CGTCGTCGCG	TAGTAACGGT
660	670	680	690	700
* *	* *	* *	* *	* *
TACTGCTGGA	CGCCCACCAT	AAGACCTACG	ACCCACCTA	CTCCGACTTC
ATGACGACCT	GCGGGTGGTA	TTCTGGATGC	TGGGGTGGAT	GAGGCTGAAG
710	720	730	740	750
* *	* *	* *	* *	* *
TGCCAGTTCC	GGCCTCCAGT	TCGTGTGAAT	GATGGTGGAG	GGAGCCATCC
ACGGTCAAGG	CCGGAGGTCA	AGCACACTTA	CTACCACCTC	CCTCGGTAGG
760	770	780	790	800
* *	* *	* *	* *	* *
TTCCAGGCCC	AACTCCAGAC	ACACTCCCAG	CTTCTCTGGG	GACTCCTCCT
AAGGTCCGGG	TTGAGGTCTG	TGTGAGGGTC	GAAGAGACCC	CTGAGGAGGA
810	820	830	840	850
* *	* *	* *	* *	* *
CCTCCTGCTC	AGATCACTGT	ATCACCTCTT	CAGACATGAT	GGACTCGTCC
GGAGGACGAG	TCTAGTGACA	TAGTGGAGAA	GTCTGTACTA	CCTGAGCAGG
860	870	880	890	900
* *	* *	* *	* *	* *
AGCTTCTCCA	ATCTGGATCT	GAGTGAAGAA	GATTCAGATG	ACCTTCTCTG
TCGAAGAGGT	TAGACCTAGA	CTCACTTCTT	CTAAGTCTAC	TGGGAAGACA
910	920	930	940	950
* *	* *	* *	* *	* *
GACCCTAGAG	CTGTCCCGAC	TCTCCATGCT	GCCCCACCTG	GCTGACCTGG
CTGGGATCTC	GACAGGGTCG	AGAGGTACGA	CGGGGTGGAC	CGACTGGACC

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FIG 7C

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960	970	980	990	1000
* *	* *	* *	* *	* *
TCAGTTACAG	CATCCAAAAG	GTCATTGGCT	TTGCTAAGAT	GATACCAGGA
AGTCAATGTC	GTAGGTTTTT	CAGTAACCGA	AACGATTCTA	CTATGGTCCT
1010	1020	1030	1040	1050
* *	* *	* *	* *	* *
TTCAGAGACC	TCACCTCTGA	GGACCAGATC	GTACTGCTGA	AGTCAAGTGC
AAGTCTCTGG	AGTGGAGACT	CCTGGTCTAG	CATGACGACT	TCAGTTCACG
1060	1070	1080	1090	1100
* *	* *	* *	* *	* *
CATTGAGGTC	ATCATGTTGC	GCTCCAATGA	GTCCCTCACC	ATGGACGACA
GTAAGTCCAG	TAGTACAACG	CGAGGTTACT	CAGGAAGTGG	TACCTGCTGT
1110	1120	1130	1140	1150
* *	* *	* *	* *	* *
TGTCCTGGAC	CTGTGGCAAC	CAAGACTACA	AGTACCGCGT	CAGTGACGTG
ACAGGACCTG	GACACCGTTG	GTTCTGATGT	TCATGGCGCA	GTCAGTGCAC
1160	1170	1180	1190	1200
* *	* *	* *	* *	* *
ACCAAAGCCG	GACACAGCCT	GGAGCTGATT	GAGCCCCTCA	TCAAGTTCCA
TGGTTTTCGC	CTGTGTCGGA	CCTCGACTAA	CTCGGGGAGT	AGTTCAAGGT
1210	1220	1230	1240	1250
* *	* *	* *	* *	* *
GGTGGGACTG	AAGAAGCTGA	ACTTGCAATG	GGAGGAGCAT	GTCCTGCTCA
CCACCCCTGAC	TTCTTCGACT	TGAACGTACT	CCTCCTCGTA	CAGGACGAGT
1260	1270	1280	1290	1300
* *	* *	* *	* *	* *
TGGCCATCTG	CATCGTCTCC	CCAGATCGTC	CTGGGGTGCA	GGACGCCGCG
ACCGGTAGAC	GTAGCAGAGG	GGTCTAGCAG	GACCCACGCT	CCTGCGGCGC
1310	1320	1330	1340	1350
* *	* *	* *	* *	* *
CTGATTGAGG	CCATCCAGGA	CCGCCTGTCC	AACACACTGC	AGACGTACAT
GACTAACTCC	GGTAGGTCCT	GGCGGACAGG	TTGTGTGACG	TCTGCATGTA
1360	1370	1380	1390	1400
* *	* *	* *	* *	* *
CCGCTGCCGC	CACCCGCCCC	CGGGCAGCCA	CCTGCTCTAT	GCCAAGATGA
GGCGACGGCG	GTGGGCGGGG	GCCCGTCGGT	GGACGAGATA	CGGTTCTACT
1410	1420	1430	1440	1450
* *	* *	* *	* *	* *
TCCAGAAGCT	AGCCGACCTG	CGCAGCCTCA	ATGAGGAGCA	CTCCAAGCAG
AGGTCTTCGA	TCGGCTGGAC	GCGTCGGAGT	TACTCCTCGT	GAGGTTCTGC
1460	1470	1480	1490	1500
* *	* *	* *	* *	* *
TACCGCTGCC	TCTCCTTCCA	GCCTGAGTGC	AGCATGAAGC	TAACGCCCCCT
ATGGCGACGG	AGAGGAAGGT	CGGACTCACG	TCGTACTTCG	ATTGCGGGGA

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FIG 7D 16/20

1510	1520	1530	
*	*	*	*
TGTGCTCGAA	GTGTTTGGCA	ATGAGATCTC	CTGA (SEQ ID NO:4)
ACACGAGCTT	CACAAACCGT	TACTCTAGAG	GACT (SEQ ID NO:19)

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FIG 8A

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FIGURE 8

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      10          20          30          40          50
      *          *          *          *          *
TGCGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
ACGCTGGAAC CGCCACTCGG ACCCTGTCC CCACTCCGGT CTCTGCCTGC

      60          70          80          90          100
      *          *          *          *          *
GACGCAGGGG CCCGGCCCAA GCGGAGGGAG AACAGCGGCA CTAAGGCAGA
CTGCGTCCCC GGGCCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT

      110         120         130         140         150
      *          *          *          *          *
AAGGAAGAGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG

      160         170         180         190         200
      *          *          *          *          *
TCCTAGACGC TGGTAGAAAG TTCCTCCGAG GAGCCTGCCA TCCAGTCGTG
AGGATCTGCG ACCATCTTTC AAGGAGGCTC CTCGGACGGT AGGTCAGCAC

      210         220         230         240         250
      *          *          *          *          *
CGTGCAGAAG CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGCTCTCTCG

      260         270         280         290         300
      *          *          *          *          *
ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
                                           MetGluAla>

      310         320         330         340         350
      *          *          *          *          *
TGGCGGCCAG CACTTCCCTG CCTGACCCTG GAGACTTTGA CCGGAACGTG
ACCGCCGGTC GTGAAGGGAC GGA CTCTGAAACT GGCCTTGAC
MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>

      360         370         380         390         400
      *          *          *          *          *
CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
GGGGCCTAGA CACCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT
ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>

      410         420         430         440         450
      *          *          *          *          *
TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTGAGGCGA AGCATGAAGC
ACGATACTGG ACACTTCCGA CGTTTCCGAA GAAGTCCGCT TCGTACTTCG
AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>

      460         470         480         490         500
      *          *          *          *          *
GGAAGGCACT ATTACCTGC CCCTTCAACG GGGACTGCCG CATCACCAAG
CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC GTAGTGGTTC
ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>

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FIG 8B

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      510      520      530      540      550
      *        *        *        *        *
GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
CTGTTGGCTG CCGTGACGGT CCGGACGGCC GAGTTTGC GA CACACCTGTA
AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

      560      570      580      590      600
      *        *        *        *        *
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

      610      620      630      640      650
      *        *        *        *        *
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
CCCTCTACTA GGA CTTCGCC TTCCTCCTCC TCCGGA ACTT CCTGT CAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

      660      670      680      690      700
      *        *        *        *        *
CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

      710      720      730      740      750
      *        *        *        *        *
CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

      760      770      780      790      800
      *        *        *        *        *
GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

      810      820      830      840      850
      *        *        *        *        *
AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

      860      870      880      890      900
      *        *        *        *        *
AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

      910      920      930      940      950
      *        *        *        *        *
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

      960      970      980      990      1000
      *        *        *        *        *
CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>

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FIG 8C

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1010      1020      1030      1040      1050
  *        *        *        *        *
CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

1060      1070      1080      1090      1100
  *        *        *        *        *
TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACCTCCAG
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

1110      1120      1130      1140      1150
  *        *        *        *        *
ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC
TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

1160      1170      1180      1190      1200
  *        *        *        *        *
CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

1210      1220      1230      1240      1250
  *        *        *        *        *
GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

1260      1270      1280      1290      1300
  *        *        *        *        *
AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

1310      1320      1330      1340      1350
  *        *        *        *        *
CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
GTAGCAGAGG GGTCTAGCAG GACCCACAGT CCTGCGGCGC GACTAACTCC
IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

1360      1370      1380      1390      1400
  *        *        *        *        *
CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
GGTAGGTCCT GGC GGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

1410      1420      1430      1440      1450
  *        *        *        *        *
CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

1460      1470      1480      1490      1500
  *        *        *        *        *
AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCTGTC ATGGCGACGG
AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>
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FIG 8D 20/20

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1510      1520      1530      1540      1550
  *          *          *          *          *
TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCCT TGTGCTCGAA
AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

1560      1570
  *          *
GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO: 7)
CACAAACCGT TACTCTAGAG GACT (SEQ ID NO: 20)
ValPheGly AsnGluIleSer ***> (SEQ ID NO: 12)
```